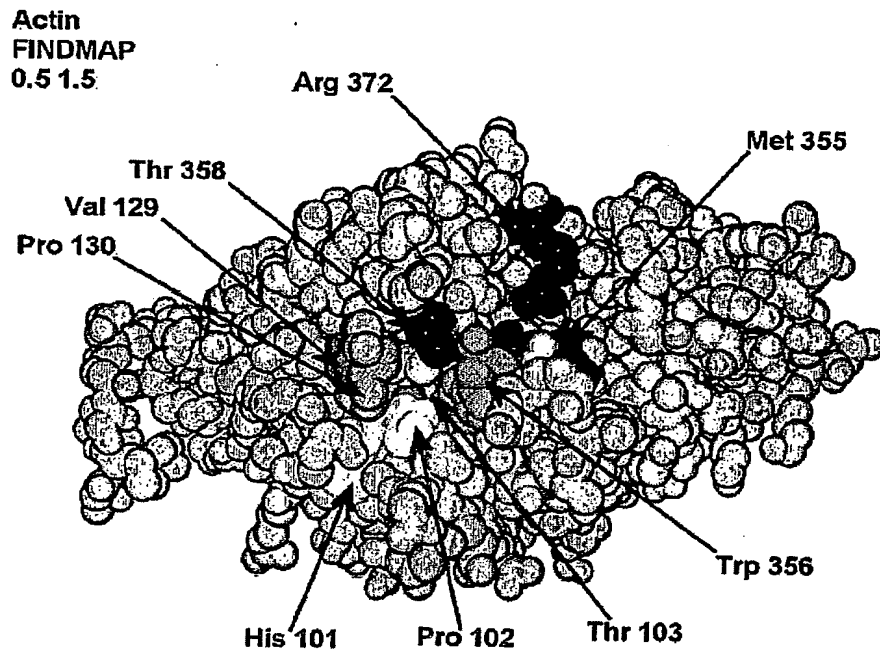


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probe residue	target residue																			
	A	C	D	E	F	G	H	I	K	L	M	N	P	Q	R	S	T	V	W	Y
A	1	0	0	0	0	0.5	0	0	0.5	0	0	0	0.5	0	0	0.5	0.25	0	0	0
C		1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
D			1	0.5	0	0	0	0	0	0	0	0.5	0	0.25	0	0	0	0	0	0
E				1	0	0	0	0	0	0	0	0.25	0	0.5	0	0	0	0	0	0
F					1	0	0	0	0	0	0	0	0	0	0	0	0	0	0.25	0.5
G						1	0	0	0	0	0	0.5	0.5	0	0	0.25	0.25	0	0	0
H							1	0	0.25	0	0	0	0	0	0.25	0	0	0	0	0
I								1	0	0.5	0.25	0	0	0	0	0	0	0.5	0	0
K									1	0	0	0	0	0.5	0.5	0	0.5	0	0	0
L										1	0.25	0	0	0	0	0	0	0.5	0	0
M											1	0	0	0	0	0	0	0.25	0	0
N												1	0	0.25	0	0	0	0	0	0
P													1	0	0	0	0	0	0	0
Q														1	0	0	0	0	0	0
R															1	0	0	0	0	0
S																1	0.5	0	0	0
T																	1	0	0	0
V																		1	0	0
W																			1	0.25
Y																				1

FIGURE 1

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DEDETTALVCDNGSGLVKA##### 1-70

345

12

HPT

VP

#####YNELRVAPEEHPTLLTEAPLNPKANREKMTQIMFETFNVPAMYVAIQAVL 71-140

SLYASGRITGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDLTDYL##### 141-210

211-280

#####APPERKYSVWIGGSILASLS 281-350

76

8

MW

R

TFQQMWITKQEYDEAGPSIVHR 351-372

FIGURE 2

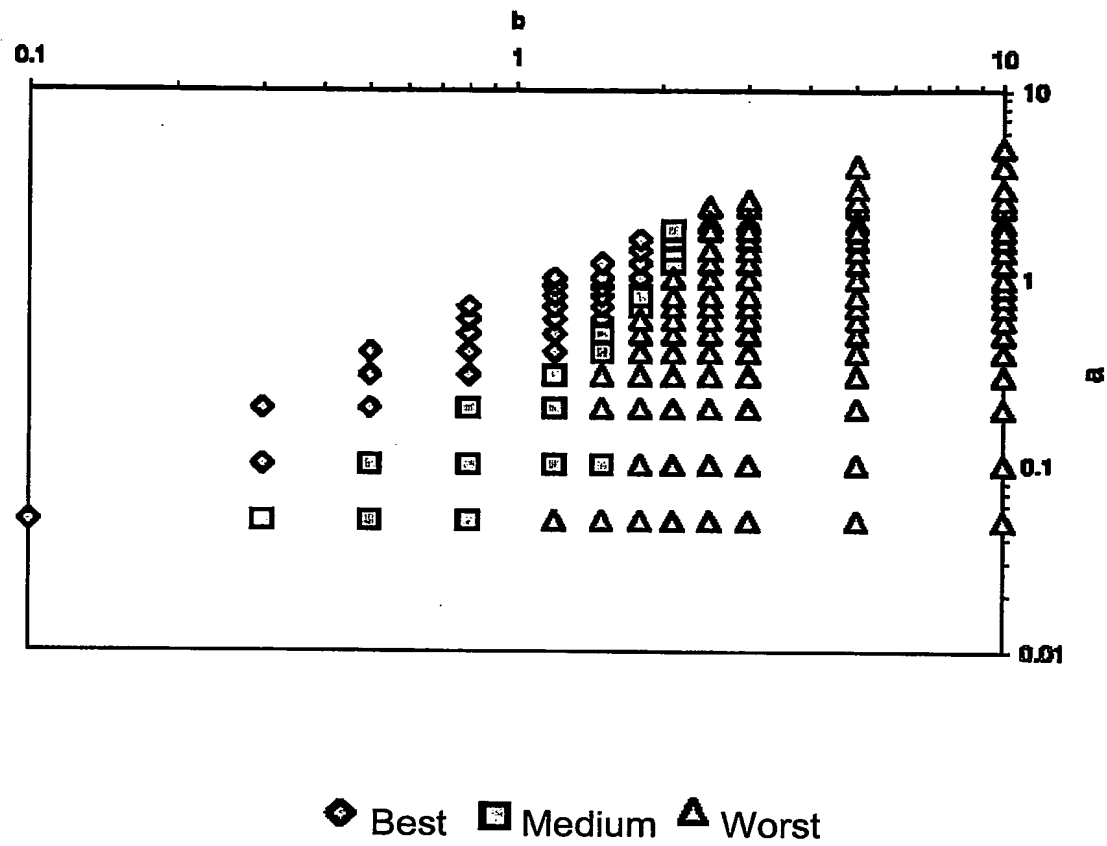


FIGURE 3

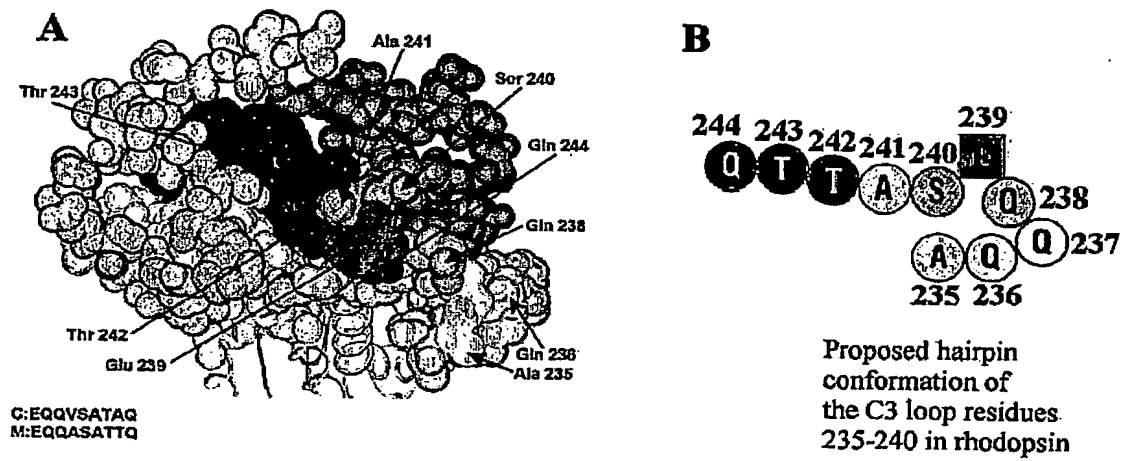


FIGURE 4

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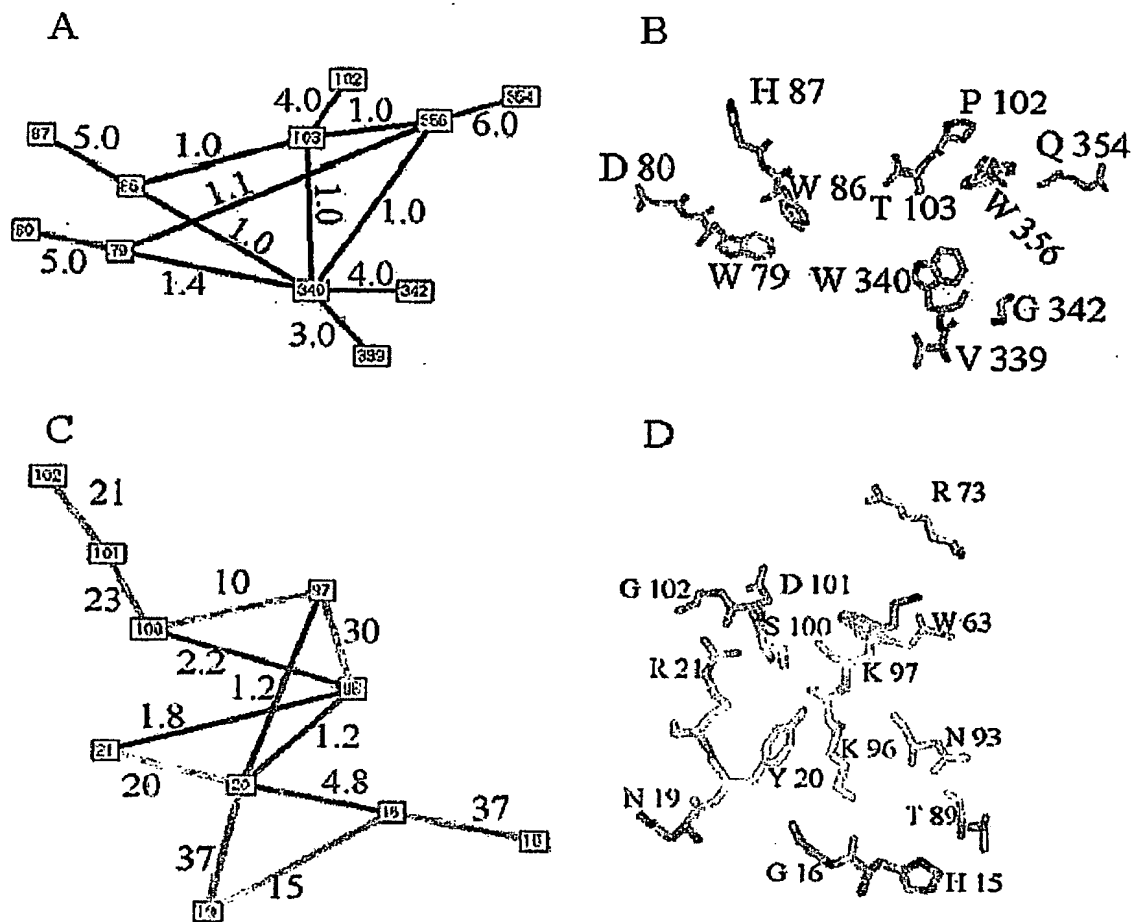


FIGURE 5